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Application Serial Number: ___10|067,122A___

Source: ___OIPE___

Date Processed by STIC: ___7|19|02___

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
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Revised 01/29/2002

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/067,122A

DATE: 07/19/2002
TIME: 14:11:12

See p. 6 for explanation of error

Input Set : A:\iu-0008.ST25.txt
Output Set: N:\CRF3\07192002\J067122A.raw

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 3 <110> APPLICANT: Kwon, Byoung S
 5 <120> TITLE OF INVENTION: Antibody for 4-1BB
 7 <130> FILE REFERENCE: 740.009US2 (IU-0008)
 9 <140> CURRENT APPLICATION NUMBER: US 10/067,122A
10 <141> CURRENT FILING DATE: 2002-02-04
12 <150> PRIOR APPLICATION NUMBER: US 08/012,269
13 <151> PRIOR FILING DATE: 1993-02-01
15 <150> PRIOR APPLICATION NUMBER: US 07/922,996
16 <151> PRIOR FILING DATE: 1992-07-30
18 <150> PRIOR APPLICATION NUMBER: US 07/267,577
19 <151> PRIOR FILING DATE: 1988-11-07
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2350
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus musculus
30 <220> FEATURE:
31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: (1253)..(1255)
33 <223> OTHER INFORMATION: n=a, c, g, or t
36 <400> SEQUENCE: 1
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39 ctacaccagg aaaaggacac attcgacaac aggaaaggag cctgtcacag aaaaccacag     120
41 tgtcctgtgc atgtgacatt tcgccatggg aaacaactgt tacaacgtgg tggtcattgt     180
43 gctgctgcta gtgggctgtg agaaggtggg agccgtgcag aactcctgtg ataactgtca     240
45 gcctggtact ttctgcagaa aatacaatcc agtctgcaag agctgccctc caagtacctt     300
47 ctccagcata ggtggacagc cgaactgtaa catctgcaga gtgtgtgcag gctatttcag     360
49 gttcaagaag ttttgctcct ctacccacaa cgcggagtgt gagtgcattg aaggattcca     420
51 ttgcttgggg ccacagtgca ccagatgtga aaaggactgc aggcctggcc aggagctaac     480
53 gaagcagggt tgcaaaacct gtagcttggg aacatttaat gaccagaacg tactggcgt     540
55 ctgtcgaccc tggacgaact gctctctaga cggaaggtct gtgcttaaga ccgggaccac     600
57 ggagaaggac gtggtgtgtg dacccctgt ggtgagcttc tctcccagta ccaccatttc     660
59 tgtgactcca gagggaggac caggagggca ctccttgcag gtccttacct tgttcctggc     720
61 gctgacatcg gctttgctgc tggccctgat cttcattact ctcctgttct ctgtgctcaa     780
63 atggatcagg aaaaaattcc cccacatatt caagcaacca tttaagaaga ccactggagc     840
65 agctcaagag gaagatgctt gtagctgccg atgtccacag gaagaagaag gaggaggagg     900
67 aggctatgag ctgtgatgta ctatcctagg agatgtgtgg gccgaaaccg agaagcacta     960
69 ggaccccacc atcctgtgga acagcacaag caaccccacc accctgttct tacacatcat    1020
71 cctagatgat gtgtgggcgc gcacctcatc caagtctctt ctaacgctaa catatttgtc    1080
73 tttacctttt ttaaatcttt ttttaaattt aaattttatg tgtgtgagtg ttttgcctgc    1140
75 ctgtatgcac acgtgtgtgt gtgtgtgtgt gtgacactcc tgatgcctga ggaggtcaga    1200
W--> 77 agagaaaggg ttggttccat aagaactgga gttatggatg gctgtgagcc ggnnngatag    1260
```

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 79 gtcgggacgg agacctgtct tcttattttta acgtgactgt ataataaaaa aaaaatgata    1320
 81 tttcgggaat tgtagagatt ctcctgacac ccttctagtt aatgatctaa gaggaattgt    1380
 83 tgatacgtag tatactgtat atgtgtatgt atatgtatat gtatatataa gactcttta     1440
 85 ctgtcaaagt caacctagag tgtctggtta ccaggtcaat tttattggac attttacgtc    1500
 87 acacacacac acacacacac acacacgt ttatactacg tactgttatc ggtattctac       1560
 89 gtcatataat gggatagggt aaaaggaaac caaagagtga gtgatattat tgtggaggtg    1620
 91 acagactacc ccttctgggt acgtagggac agacctcctt cggactgtct aaaactcccc    1680
 93 ttagaagtct cgtcaagttc ccggacgaag aggacagagg agacacagtc cgaaaagtta    1740
 95 tttttccggc aaatcctttc cctgtttcgt gacactccac cccttgtgga cacttgagtg    1800
 97 tcatccttgc gccggaaggt caggtggtac ccgtctgtag gggcggggag acagagccgc    1860
 99 gggggagcta cgagaatcga ctcacagggc gccccgggct tcgcaaatga aactttttta    1920
101 atctcacaag tttcgtccgg gctcggcgga cctatggcgt cgatccttat taccttatcc     1980
103 tggcgccaag ataaacaac caaaagccct gactccggta ctaattctcc ctgccggccc      2040
105 ccgtaagcat aacgcggcga tctccacttt aagaacctgg ccgcgttctg cctggtctcg     2100
107 ctttcgtaaa cggttcttac aaaagtaatt agttcttgct ttcagcctcc aagcttctgc     2160
109 tagtctatgg cagcatcaag gctggtattt gctacggctg accgctacgc cgccgcaata    2220
111 agggtactgg gcggcccgtc gaaggccctt tggtttcaga aacccaaggc ccccctcata    2280
113 ccaacgtttc gactttgatt cttgccggta cgtggtggtg ggtgccttag ctctttctcg    2340
115 atagttagac                                                            2350
118 <210> SEQ ID NO: 2
119 <211> LENGTH: 256
120 <212> TYPE: PRT
121 <213> ORGANISM: Mus musculus
123 <400> SEQUENCE: 2
125 Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
126 1               5                   10                  15
129 Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
130             20                  25                  30
133 Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
134             35                  40                  45
137 Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
138         50                  55                  60
141 Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
142 65                  70                  75                  80
145 His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
146             85                  90                  95
149 Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
150             100                 105                 110
153 Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
154             115                 120                 125
157 Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
158         130                 135                 140
161 Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
162 145                 150                 155                 160
165 Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
166             165                 170                 175
169 Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala
170             180                 185                 190
173 Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
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Input Set : A:\iu-0008.ST25.txt
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```
174          195              200              205
177 Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
178     210              215              220
181 Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
182 225              230              235              240
185 Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu
186              245              250              255
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 24
191 <212> TYPE: PRT
192 <213> ORGANISM: Mus musculus
194 <400> SEQUENCE: 3
196 Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser
197 1              5              10              15
200 Thr His Asn Ala Glu Cys Glu Cys
201              20
204 <210> SEQ ID NO: 4
205 <211> LENGTH: 22
206 <212> TYPE: PRT
207 <213> ORGANISM: Drosophila
209 <400> SEQUENCE: 4
211 Cys Pro Val Cys Phe Asp Tyr Val Ile Leu Gln Cys Ser Ser Gly His
212 1              5              10              15
215 Leu Val Cys Val Ser Cys
216              20
219 <210> SEQ ID NO: 5
220 <211> LENGTH: 26
221 <212> TYPE: PRT
222 <213> ORGANISM: Dictyostelium
224 <400> SEQUENCE: 5
226 Cys Pro Ile Cys Phe Glu Phe Ile Tyr Lys Lys Gln Ile Tyr Gln Cys
227 1              5              10              15
230 Lys Ser Gly His His Ala Cys Lys Glu Cys
231              20              25
234 <210> SEQ ID NO: 6
235 <211> LENGTH: 6
236 <212> TYPE: PRT
237 <213> ORGANISM: Mus musculus
239 <220> FEATURE:
240 <221> NAME/KEY: MISC_FEATURE
241 <222> LOCATION: (5)..(5)
242 <223> OTHER INFORMATION: X=any amino acid
245 <400> SEQUENCE: 6
W--> 247 Val Gln Asn Ser Xaa Asp
248 1              5
251 <210> SEQ ID NO: 7
252 <211> LENGTH: 12
253 <212> TYPE: PRT
C--> 254 <213> ORGANISM: Artificial
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Input Set : A:\iu-0008.ST25.txt
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```
W--> 256 <220> FEATURE:
W--> 256 <223> OTHER INFORMATION:
     256 <400> SEQUENCE: 7
     258 Cys Arg Pro Gly Gln Glu Leu Thr Lys Ser Gly Tyr
     259 1               5                   10
     262 <210> SEQ ID NO: 8
     263 <211> LENGTH: 24
     264 <212> TYPE: PRT
C--> 265 <213> ORGANISM: artificial
     267 <220> FEATURE:
     268 <221> NAME/KEY: MISC_FEATURE
     269 <222> LOCATION: (2)..(3)
     270 <223> OTHER INFORMATION: X=any amino acid
     273 <220> FEATURE:
     274 <221> NAME/KEY: MISC_FEATURE
     275 <222> LOCATION: (5)..(13)
     276 <223> OTHER INFORMATION: X=any amino acid
     279 <220> FEATURE:
     280 <221> NAME/KEY: MISC_FEATURE
     281 <222> LOCATION: (15)..(17)
     282 <223> OTHER INFORMATION: X=any amino acid
     285 <220> FEATURE:
     286 <221> NAME/KEY: MISC_FEATURE
     287 <222> LOCATION: (19)..(21)
     288 <223> OTHER INFORMATION: X=any amino acid
     291 <220> FEATURE:
     292 <221> NAME/KEY: MISC_FEATURE
     293 <222> LOCATION: (23)..(23)
     294 <223> OTHER INFORMATION: X=any amino acid
     297 <400> SEQUENCE: 8
W--> 299 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
     300 1               5                   10                  15
W--> 303 Xaa His Xaa Xaa Xaa Cys Xaa Cys
     304             20
     307 <210> SEQ ID NO: 9
     308 <211> LENGTH: 4
     309 <212> TYPE: PRT
C--> 310 <213> ORGANISM: Artificial
W--> 312 <220> FEATURE:
W--> 312 <223> OTHER INFORMATION:
     312 <400> SEQUENCE: 9
     314 Cys Arg Cys Pro
     315 1
     318 <210> SEQ ID NO: 10
     319 <211> LENGTH: 4
     320 <212> TYPE: PRT
C--> 321 <213> ORGANISM: Artificial
     323 <220> FEATURE:
     324 <221> NAME/KEY: MISC_FEATURE
```

```
      325 <222> LOCATION: (2)..(2)
      326 <223> OTHER INFORMATION: X=any amino acid
      329 <400> SEQUENCE: 10
W--> 331 Cys Xaa Cys Pro
      332 1
      335 <210> SEQ ID NO: 11
      336 <211> LENGTH: 25
      337 <212> TYPE: DNA
C--> 338 <213> ORGANISM: Artificial
W--> 340 <220> FEATURE:
W--> 340 <223> OTHER INFORMATION:
      340 <400> SEQUENCE: 11
      341 acctcgaggt cctgtgcatg tgaca                              25
      344 <210> SEQ ID NO: 12
      345 <211> LENGTH: 25
      346 <212> TYPE: DNA
C--> 347 <213> ORGANISM: Artificial
W--> 349 <220> FEATURE:
W--> 349 <223> OTHER INFORMATION:
      349 <400> SEQUENCE: 12
      350 atgaattctt actgcaggag tgccc                              25
      353 <210> SEQ ID NO: 13
      354 <211> LENGTH: 11
      355 <212> TYPE: PRT
      356 <213> ORGANISM: Mus musculus
      358 <400> SEQUENCE: 13
      360 Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly
      361 1               5                   10
```

```
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Input Set : A:\iu-0008.ST25.txt
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```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1253,1254,1255
Seq#:6; Xaa Pos. 5
Seq#:8; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,15,16,17,19,20,21,23
Seq#:10; Xaa Pos. 2

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:7,9,11,12

VERIFICATION SUMMARY   DATE: 07/19/2002
PATENT APPLICATION: **US/10/067,122A**   TIME: 14:11:13

Input Set : **A:\iu-0008.ST25.txt**
Output Set: **N:\CRF3\07192002\J067122A.raw**

```
L:77  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1200
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:254 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:256 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:256 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:265 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:16
L:310 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:312 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:312 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:321 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:338 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:340 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:340 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:347 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:349 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:349 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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